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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=2; day=15; hr=12; min=18; sec=18; ms=279;]
=====

Reviewer Comments:

<400> 3

Met Ala Ser Pro Arg Glu Leu Thr Gln Asn Pro Leu Lys Lys Ile

1

5

10

15

Trp Met Pro Tyr Ser Asn Gly Arg Pro Ala Leu His Ala Cys Gln

20

25

30

Please remove the blank line between the amino acids and their
respective numbers above. This error appears in subsequent amino acid
sequences. Also, please remove the blank lines between rows of
nucleotides (this appears in subsequent sequences).

(end of Sequence 86)

ttttatttta tttatttttt gatggagtct tgcactccag cctggtgaca gact 1914

PF-1506 PCT

1/94

WASH_1695548.1

Please remove the above three lines of text, which appear at the end of
the submitted file.

Application No: 10554917

Version No: 1.0

Input Set:

Output Set:

Started: 2008-02-14 12:58:35.910

Finished: 2008-02-14 12:58:45.206

Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 296 ms

Total Warnings: 4

Total Errors: 58

No. of SeqIDs Defined: 86

Actual SeqID Count: 86

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SeqID (3)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SeqID (5)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SeqID (7)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SeqID (9)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SeqID (11)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SeqID (11)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SeqID (11)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SeqID (13)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SeqID (15)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SeqID (16)

Input Set:

Output Set:

Started: 2008-02-14 12:58:35.910
Finished: 2008-02-14 12:58:45.206
Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 296 ms
Total Warnings: 4
Total Errors: 58
No. of SeqIDs Defined: 86
Actual SeqID Count: 86

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (22)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (22)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (23)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (24)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (26)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (26)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (28)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (29)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (31)
E 355	Empty lines found between the amino acid numbering and the proteins
E 321	No. of Bases conflict, this line has no nucleotides SEQID (31) POS (915)
E 330	Invalid protein , found in SEQID(86) POS (1)Invalid Protein:PCI

Input Set:

Output Set:

Started: 2008-02-14 12:58:35.910
Finished: 2008-02-14 12:58:45.206
Elapsed: 0 hr(s) 0 min(s) 9 sec(s) 296 ms
Total Warnings: 4
Total Errors: 58
No. of SeqIDs Defined: 86
Actual SeqID Count: 86

Error code	Error Description
W 112	Upper case found in data; Found at position(1914) SeqId(86)
W 112	Upper case found in data; Found at position(1915) SeqId(86)
W 112	Upper case found in data; Found at position(1916) SeqId(86)
W 112	Upper case found in data; Found at position(1917) SeqId(86)
E 259	Found undefined lettercode; POS (1919) SEQID(86)
E 259	Found undefined lettercode; POS (1920) SEQID(86)
E 259	Found undefined lettercode; POS (1921) SEQID(86)
E 259	Found undefined lettercode; POS (1922) SEQID(86)
E 259	Found undefined lettercode; POS (1923) SEQID(86)
E 259	Found undefined lettercode; POS (1924) SEQID(86)
E 259	Found undefined lettercode; POS (1925) SEQID(86)
E 259	Found undefined lettercode; POS (1926) SEQID(86)
E 259	Found undefined lettercode; POS (1927) SEQID(86)
E 254	The total number of bases conflicts with running total, Input: 1, Calculated : 1927 SEQID(86)
E 253	The number of bases differs from <211> Input: 1914 Calculated:1927 SEQID (86)

<110> INCYTE CORPORATION; ELLIOTT, Vicki S.;
 KHARE, Reena; RICHARDSON, Thomas W.;
 MARQUIS, Joseph P.; SWARNIAKAR, Anita;
 HAFALTA, April J.A.; BECHA, Shanya D.;
 CHAWLA, Harinder K.; BADGH, Mariah R.;
 LEE, Soo Yeun; TRAN, Uyen K.;
 YUE, Henry; NGUYEN, Denniel B.;
 THORNTON, Michael B.; GURURAJAN, Rajagopal;
 GANDHI, Ameena R.; LU, Yan;
 YAO, Monique G.; LI, Joana X.;
 LUO, Wen; LEE, Ernestine A.;
 FORSYTHE, Ian J.; ISCH, Craig H.;
 WILSON, Amy D.; JIN, Pei

<120> KINASES AND PHOSPHATASES

<130> PF-1506 PCT

<140> 10554917

<141> 2008-02-14

<150> US 60/467,491

<151> 2003-04-30

<150> US 60/469,441

<151> 2003-05-09

<150> US 60/476,408

<151> 2003-06-05

<150> US 60/494,656

<151> 2003-08-12

<150> US 60/524,415

<151> 2003-11-20

<150> US 60/528,750

<151> 2003-12-10

<160> 86

<170> PERL Program

<210> 1

<211> 83

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7517831CD1

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Met	Gly	Cys	Gly	Cys	Ser	Ser	His	Pro	Glu	Asp	Asp	Trp	Met	Glu
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Asn	Ile	Asp	Val	Cys	Glu	Asn	Cys	His	Tyr	Pro	Ile	Val	Pro	Leu
				20					25					30

Asp	Gly	Lys	Gly	Thr	Leu	Leu	Ile	Arg	Asn	Gly	Ser	Glu	Thr	Thr	
				35					40						45
Trp	Leu	Ser	Leu	Cys	Thr	Ala	Met	Ser	Pro	Leu	Thr	Thr	Glu	Ile	
				50					55						60
Trp	Ala	Leu	Arg	Arg	Gly	Asn	Ser	Ser	Ala	Ser	Trp	Ser	Arg	Ala	
				65					70						75
Ala	Ser	Gly	Gly	Arg	Arg	Ser	Pro								
				80											

<210> 2

<211> 292

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7520272CD1

<400> 2

Met	Ala	Asp	Gln	Ala	Pro	Phe	Asp	Thr	Asp	Val	Asn	Thr	Leu	Thr	
1				5					10						15
Arg	Phe	Val	Met	Glu	Glu	Gly	Arg	Lys	Ala	Arg	Gly	Thr	Gly	Glu	
				20					25						30
Leu	Thr	Gln	Leu	Leu	Asn	Ser	Leu	Cys	Thr	Ala	Val	Lys	Ala	Ile	
				35					40						45
Ser	Ser	Ala	Val	Arg	Lys	Ala	Gly	Ile	Ala	His	Leu	Tyr	Gly	Ile	
				50					55						60
Ala	Gly	Ser	Thr	Asn	Val	Thr	Gly	Asp	Gln	Val	Lys	Lys	Leu	Asp	
				65					70						75
Val	Leu	Ser	Asn	Asp	Leu	Val	Met	Asn	Met	Leu	Lys	Ser	Ser	Phe	
				80					85						90
Ala	Thr	Cys	Val	Leu	Val	Ser	Glu	Glu	Asp	Lys	His	Ala	Ile	Ile	
				95					100						105
Val	Glu	Pro	Glu	Lys	Arg	Gly	Lys	Tyr	Val	Val	Cys	Phe	Asp	Pro	
				110					115						120
Leu	Asp	Gly	Ser	Ser	Asn	Ile	Asp	Cys	Leu	Val	Ser	Val	Gly	Thr	
				125					130						135
Ile	Phe	Gly	Ile	Tyr	Arg	Lys	Lys	Ser	Thr	Asp	Glu	Pro	Ser	Glu	
				140					145						150
Lys	Asp	Ala	Leu	Gln	Pro	Gly	Arg	Asn	Leu	Val	Ala	Ala	Gly	Tyr	
				155					160						165
Ala	Leu	Tyr	Gly	Ser	Ala	Thr	Met	Leu	Val	Leu	Ala	Met	Asp	Cys	
				170					175						180
Gly	Val	Asn	Cys	Phe	Met	Leu	Asp	Pro	Asp	Asn	Ser	Ala	Pro	Tyr	
				185					190						195
Gly	Ala	Arg	Tyr	Val	Gly	Ser	Met	Val	Ala	Asp	Val	His	Arg	Thr	
				200					205						210
Leu	Val	Tyr	Gly	Gly	Ile	Phe	Leu	Tyr	Pro	Ala	Asn	Lys	Lys	Ser	
				215					220						225
Pro	Asn	Gly	Lys	Leu	Arg	Leu	Leu	Tyr	Glu	Cys	Asn	Pro	Met	Ala	
				230					235						240
Tyr	Val	Met	Glu	Lys	Ala	Gly	Gly	Met	Ala	Thr	Thr	Gly	Lys	Glu	
				245					250						255
Ala	Val	Leu	Asp	Val	Ile	Pro	Thr	Asp	Ile	His	Gln	Arg	Ala	Pro	
				260					265						270
Val	Ile	Leu	Gly	Ser	Pro	Asp	Asp	Val	Leu	Glu	Phe	Leu	Lys	Val	
				275					280						285

Tyr Glu Lys His Ser Ala Gln
290

<210> 3
<211> 434
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<223> Incyte ID No: 7521279CD1

<400> 3
Met Ala Ser Pro Arg Glu Leu Thr Gln Asn Pro Leu Lys Lys Ile
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Trp Met Pro Tyr Ser Asn Gly Arg Pro Ala Leu His Ala Cys Gln
20 25 30
Arg Gly Val Cys Met Thr Asn Cys Pro Thr Leu Ile Val Met Val
35 40 45
Gly Leu Pro Ala Arg Gly Lys Thr Tyr Ile Ser Lys Lys Leu Thr
50 55 60
Arg Tyr Leu Asn Trp Ile Gly Val Pro Thr Arg Glu Phe Asn Val
65 70 75
Gly Gln Tyr Arg Asp Val Val Lys Thr Tyr Lys Ser Phe Glu
80 85 90
Phe Phe Leu Pro Asp Asn Glu Glu Gly Leu Lys Ile Arg Lys Gln
95 100 105
Cys Ala Leu Ala Ala Leu Arg Asp Val Arg Arg Phe Leu Ser Glu
110 115 120
Glu Gly Gly His Val Ala Val Phe Asp Ala Thr Asn Thr Thr Arg
125 130 135
Glu Arg Arg Ala Thr Ile Phe Asn Phe Gly Glu Gln Asn Gly Tyr
140 145 150
Lys Thr Phe Phe Val Glu Ser Ile Cys Val Asp Pro Glu Val Ile
155 160 165
Ala Ala Asn Ile Val Gln Val Lys Leu Gly Ser Pro Asp Tyr Val
170 175 180
Asn Arg Asp Ser Asp Glu Ala Thr Glu Asp Phe Met Arg Arg Ile
185 190 195
Glu Cys Tyr Glu Asn Ser Tyr Glu Ser Leu Asp Glu Asp Leu Asp
200 205 210
Arg Asp Leu Ser Tyr Ile Lys Ile Met Asp Val Gly Gln Ser Tyr
215 220 225
Val Val Asn Arg Val Ala Asp His Ile Gln Ser Arg Ile Val Tyr
230 235 240
Tyr Leu Met Asn Ile His Val Thr Pro Arg Ser Ile Tyr Leu Cys
245 250 255
Arg His Gly Glu Ser Glu Leu Asn Leu Lys Gly Arg Ile Gly Gly
260 265 270
Asp Pro Gly Leu Ser Pro Arg Gly Arg Glu Phe Ala Lys Ser Leu
275 280 285
Ala Gln Phe Ile Ser Asp Gln Asn Ile Lys Asp Leu Lys Val Trp
290 295 300
Thr Ser Gln Met Lys Arg Thr Ile Gln Thr Ala Glu Ala Leu Gly
305 310 315
Val Pro Tyr Glu Gln Trp Lys Val Leu Asn Glu Ile Asp Ala Ser

	320	325	330
Tyr Glu Asp Leu Val Gln Arg Leu Glu Pro Val Ile Met Glu Leu			
	335	340	345
Glu Arg Gln Glu Asn Val Leu Val Ile Cys His Gln Ala Val Met			
	350	355	360
Arg Cys Leu Leu Ala Tyr Phe Leu Asp Lys Ala Ala Glu Gln Leu			
	365	370	375
Pro Tyr Leu Lys Cys Pro Leu His Thr Val Leu Lys Leu Thr Pro			
	380	385	390
Val Ala Tyr Gly Cys Lys Val Glu Ser Ile Phe Leu Asn Val Ala			
	395	400	405
Ala Val Asn Thr His Arg Asp Arg Pro Gln Asn Val Asp Ile Ser			
	410	415	420
Arg Pro Pro Glu Glu Ala Leu Val Thr Val Pro Ala His Gln			
	425	430	

<210> 4

<211> 240

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7523965CD1

<400> 4

Met Ala Ala Leu Tyr Arg Pro Gly Leu Arg Leu Asn Trp His Gly		
1	5	10
Leu Ser Pro Leu Gly Trp Pro Ser Cys Arg Ser Ile Gln Thr Leu		
20	25	30
Arg Val Leu Ser Gly Asp Leu Gly Gln Leu Pro Thr Gly Ile Arg		
35	40	45
Asp Phe Val Glu His Ser Ala Arg Leu Cys Gln Pro Glu Gly Ile		
50	55	60
His Ile Cys Asp Gly Thr Glu Ala Glu Asn Thr Ala Thr Leu Thr		
65	70	75
Leu Leu Glu Gln Gly Leu Ile Arg Lys Leu Pro Lys Tyr Asn		
80	85	90
Asn Cys Trp Leu Ala Arg Thr Asp Pro Lys Asp Val Ala Arg Val		
95	100	105
Glu Ser Lys Thr Val Ile Val Thr Pro Ser Gln Arg Asp Thr Val		
110	115	120
Pro Leu Pro Pro Gly Gly Ala Arg Gly Gln Leu Gly Asn Trp Met		
125	130	135
Ser Pro Ala Asp Phe Gln Arg Ala Val Asp Glu Arg Phe Pro Gly		
140	145	150
Cys Met Gln Gly Arg Thr Met Tyr Val Leu Pro Phe Ser Met Gly		
155	160	165
Pro Val Gly Ser Pro Leu Ser Arg Ile Gly Val Gln Leu Thr Asp		
170	175	180
Ser Ala Tyr Val Val Ala Ser Met Arg Ile Met Thr Arg Leu Gly		
185	190	195
Thr Pro Val Leu Gln Ala Leu Gly Asp Gly Asp Phe Val Lys Cys		
200	205	210
Leu His Ser Val Gly Gln Pro Leu Thr Gly Gln Asp Pro Gly His		
215	220	225
His Gln Pro Cys Arg Glu Glu Ala Leu Cys Gly Ser Arg Leu Pro		

<210> 5
 <211> 199
 <212> PRT
 <213> Homo sapiens

<220>
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 1 5 10 15
 Thr Asn Ser Pro Thr Met Val Ile Met Val Gly Leu Pro Ala Arg
 20 25 30
 Gly Lys Thr Tyr Ile Ser Thr Lys Leu Thr Arg Tyr Leu Asn Trp
 35 40 45
 Ile Gly Thr Pro Thr Lys Val Phe Asn Leu Gly Gln Tyr Arg Arg
 50 55 60
 Glu Ala Val Ser Tyr Lys Asn Tyr Glu Phe Phe Leu Pro Asp Asn
 65 70 75
 Met Glu Ala Leu Gln Ile Arg Lys Gln Cys Ala Leu Ala Ala Leu
 80 85 90
 Lys Asp Val His Asn Tyr Leu Ser His Glu Glu Gly His Val Ala
 95 100 105
 Val Phe Asp Ala Thr Asn Thr Thr Arg Glu Arg Arg Ser Leu Ile
 110 115 120
 Leu Gln Phe Ala Lys Glu His Gly Tyr Lys Val Phe Phe Ile Glu
 125 130 135
 Ser Ile Cys Asn Asp Pro Gly Ile Ile Ala Glu Asn Ile Arg Gln
 140 145 150
 Val Lys Leu Gly Ser Pro Asp Tyr Ile Asp Cys Asp Arg Glu Lys
 155 160 165
 Val Leu Glu Asp Phe Leu Lys Arg Ile Glu Cys Tyr Glu Val Asn
 170 175 180
 Tyr Gln Pro Leu Asp Glu Glu Leu Asp Arg Ser Ser Thr Trp Ala
 185 190 195
 His Ala Thr Trp

<210> 6
 <211> 406
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID No: 7524680CD1

<400> 6
 Met Glu Glu Lys Thr Ser Arg Ile Lys Val Phe Asn Leu Gly Gln
 1 5 10 15
 Tyr Arg Arg Glu Ala Val Ser Tyr Lys Asn Tyr Glu Phe Phe Leu
 20 25 30

Pro Asp Asn Met Glu Ala Leu Gln Ile Arg Lys Gln Cys Ala Leu	35	40	45
Ala Ala Leu Lys Asp Val His Asn Tyr Leu Ser His Glu Glu Gly	50	55	60
His Val Ala Val Phe Asp Ala Thr Asn Thr Thr Arg Glu Arg Arg	65	70	75
Ser Leu Ile Leu Gln Phe Ala Lys Glu His Gly Tyr Lys Val Phe	80	85	90
Phe Ile Glu Ser Ile Cys Asn Asp Pro Gly Ile Ile Ala Glu Asn	95	100	105
Ile Arg Gln Val Lys Leu Gly Ser Pro Asp Tyr Ile Asp Cys Asp	110	115	120
Arg Glu Lys Val Leu Glu Asp Phe Leu Lys Arg Ile Glu Cys Tyr	125	130	135
Glu Val Asn Tyr Gln Pro Leu Asp Glu Glu Leu Asp Ser His Leu	140	145	150
Ser Tyr Ile Lys Ile Phe Asp Val Gly Thr Arg Tyr Met Val Asn	155	160	165
Arg Val Gln Asp His Ile Gln Ser Arg Thr Val Tyr Tyr Leu Met	170	175	180
Asn Ile His Val Thr Pro Arg Ser Ile Tyr Leu Cys Arg His Gly	185	190	195
Glu Ser Glu Leu Asn Ile Arg Gly Arg Ile Gly Gly Asp Ser Gly	200	205	210
Leu Ser Val Arg Gly Lys Gln Tyr Ala Tyr Ala Leu Ala Asn Phe	215	220	225
Ile Gln Ser Gln Gly Ile Ser Ser Leu Lys Val Trp Thr Ser His	230	235	240
Met Lys Arg Thr Ile Gln Thr Ala Glu Ala Leu Gly Val Pro Tyr	245	250	255
Glu Gln Trp Lys Ala Leu Asn Glu Ile Asp Ala Gly Val Cys Glu	260	265	270
Glu Met Thr Tyr Glu Glu Ile Gln Glu His Tyr Pro Glu Glu Phe	275	280	285
Ala Leu Arg Asp Gln Asp Lys Tyr Arg Tyr Arg Tyr Pro Lys Gly	290	295	300
Glu Ser Tyr Glu Asp Leu Val Gln Arg Leu Glu Pro Val Ile Met	305	310	315
Glu Leu Glu Arg Gln Glu Asn Val Leu Val Ile Cys His Gln Ala	320	325	330
Val Met Arg Cys Leu Leu Ala Tyr Phe Leu Asp Lys Ser Ser Asp	335	340	345
Glu Leu Pro Tyr Leu Lys Cys Pro Leu His Thr Val Leu Lys Leu	350	355	360
Thr Pro Val Ala Tyr Gly Cys Lys Val Glu Ser Ile Tyr Leu Asn	365	370	375
Val Glu Thr Val Asn Thr His Arg Glu Lys Pro Glu Asn Val Asp	380	385	390
Ile Thr Arg Glu Pro Glu Glu Ala Leu Asp Thr Val Pro Ala His	395	400	405

Tyr

<210> 7

<211> 426

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID No: 7524757CD1

<400> 7

Met	Glu	Glu	Lys	Thr	Ser	Arg	Ile	Lys	Ala	Ser	Ile	Pro	Gln	Phe
1			5						10					15
Thr	Asn	Ser	Pro	Thr	Met	Val	Ile	Met	Val	Gly	Leu	Pro	Ala	Arg
				20					25					30
Gly	Lys	Thr	Tyr	Ile	Ser	Thr	Lys	Leu	Thr	Arg	Tyr	Leu	Asn	Trp
			35						40					45
Ile	Gly	Thr	Pro	Thr	Lys	Asp	Asn	Met	Glu	Ala	Leu	Gln	Ile	Arg
			50						55					60
Lys	Gln	Cys	Ala	Leu	Ala	Ala	Leu	Lys	Asp	Val	His	Asn	Tyr	Leu
			65						70					75
Ser	His	Glu	Glu	Gly	His	Val	Ala	Val	Phe	Asp	Ala	Thr	Asn	Thr
			80						85					90
Thr	Arg	Glu	Arg	Arg	Ser	Leu	Ile	Leu	Gln	Phe	Ala	Lys	Glu	His
			95						100					105
Gly	Tyr	Lys	Val	Phe	Phe	Ile	Glu	Ser	Ile	Cys	Asn	Asp	Pro	Gly
			110						115					120
Ile	Ile	Ala	Glu	Asn	Ile	Arg	Gln	Val	Lys	Leu	Gly	Ser	Pro	Asp
			125						130					135
Tyr	Ile	Asp	Cys	Asp	Arg	Glu	Lys	Val	Leu	Glu	Asp	Phe	Leu	Lys
			140						145					150
Arg	Ile	Glu	Cys	Tyr	Glu	Val	Asn	Tyr	Gln	Pro	Leu	Asp	Glu	Glu
			155						160					165
Leu	Asp	Ser	His	Leu	Ser	Tyr	Ile	Lys	Ile	Phe	Asp	Val	Gly	Thr
			170						175					180
Arg	Tyr	Met	Val	Asn	Arg	Val	Gln	Asp	His	Ile	Gln	Ser	Arg	Thr
			185						190					195
Val	Tyr	Tyr	Leu	Met	Asn	Ile	His	Val	Thr	Pro	Arg	Ser	Ile	Tyr
			200						205					210
Leu	Cys	Arg	His	Gly	Glu	Ser	Glu	Leu	Asn	Ile	Arg	Gly	Arg	Ile
			215						220					225
Gly	Gly	Asp	Ser	Gly	Leu	Ser	Val	Arg	Gly	Lys	Gln	Tyr	Ala	Tyr
			230						235					240
Ala	Leu	Ala	Asn	Phe	Ile	Gln	Ser	Gln	Gly	Ile	Ser	Ser	Leu	Lys
			245						250					255
Val	Trp	Thr	Ser	His	Met	Lys	Arg	Thr	Ile	Gln	Thr	Ala	Glu	Ala
			260						265					270
Leu	Gly	Val	Pro	Tyr	Glu	Gln	Trp	Lys	Ala	Leu	Asn	Glu	Ile	Asp
			275						280					285
Ala	Gly	Val	Cys	Glu	Glu	Met	Thr	Tyr	Glu	Glu	Ile	Arg	Glu	His
			290						295					300
Tyr	Pro	Glu	Glu	Phe	Ala	Leu	Arg	Asp	Gln	Asp	Lys	Tyr	Arg	Tyr
			305						310					315
Arg	Tyr	Pro	Lys	Gly	Glu	Ser	Tyr	Glu	Asp	Leu	Val	Gln	Arg	Leu
			320						325					330
Glu	Pro	Val	Ile	Met	Glu	Leu	Glu							